

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/277,401

DATE: 04/13/1999
TIME: 12:59:39

INPUT SET: S31404.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4 (i) APPLICANT: Jaye, Michael C.
5 Doan, Kim-Anh T.
6 Krawiec, John A.
7 Lynch, Kevin J.
8 Amin, Dilip V.
9 South, Victoria J.
10 Marchadier, Dawn
11 Maugeais, Cyrille
12 Rader, Daniel J.
13 (ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EFFECTING THE
14 LEVELS OF HIGH DENSITY LIPOPROTEIN (HDL) CHOLESTEROL AND
15 APOLIPOPROTEIN AI, VERY LOW DENSITY LIPOPROTEIN (VLDL)
16 CHOLESTEROL AND LOW DENSITY LIPOPROTEIN (LDL) CHOLESTEROL
17 (iii) NUMBER OF SEQUENCES: 31
18 (iv) CORRESPONDENCE ADDRESS:
19 (A) ADDRESSEE: Synnestvedt & Lechner LLP
20 (B) STREET: Suite 2600 Aramark Tower, 1101 Market Street
21 (C) CITY: Philadelphia
22 (D) STATE: PA
23 (E) COUNTRY: USA
24 (F) ZIP: 19107
25 (v) COMPUTER READABLE FORM:
26 (A) MEDIUM TYPE: Floppy disk
27 (B) COMPUTER: IBM PC compatible
28 (C) OPERATING SYSTEM: PC-Windows 95
29 (D) SOFTWARE: Corel WordPerfect 8.0 converted to ASCII
30 (vi) CURRENT APPLICATION DATA:
31 (A) APPLICATION NUMBER:
32 (B) FILING DATE:
33 (C) CLASSIFICATION:
34 (viii) ATTORNEY/AGENT INFORMATION:
35 (A) NAME: Kelly, Ph.D., Patrick J.
36 (B) REGISTRATION NUMBER: 34,638
37 (C) REFERENCE/DOCKET NUMBER: 22,944 USA
38 (ix) TELECOMMUNICATION INFORMATION:
39 (A) TELEPHONE: (215)923-4466
40 (B) TELEFAX: (215)923-2189
41 (2) INFORMATION FOR SEQ ID NO:1:
42 (i) SEQUENCE CHARACTERISTICS:
43 (A) LENGTH: 367 base pairs
44 (B) TYPE: nucleic acid
45 (C) STRANDEDNESS: double
46 (D) TOPOLOGY: linear

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47 (ii) MOLECULE TYPE: cDNA
48 (ix) FEATURE:
49 (A) NAME/KEY: CDS
50 (B) LOCATION: 22..180
51 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
52 GAATTCGGCT TGATCAATCG C TTC AAA AAG GGG ATC TGT CTG AGC TGC CGC 51
53 Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg
54 1 5 10
55 AAG AAC CGT TGT AAT AGC ATT GGC TAC AAT GCC AAG AAA ATG AGG AAC 99
56 Lys Asn Arg Cys Asn Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn
57 15 20 25
58 AAG AGG AAC AGC AAA ATG TAC CTA AAA ACC CGG GCA GGC ATG CCT TTC 147
59 Lys Arg Asn Ser Lys Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe
60 30 35 40
61 AGA GGT AAC CTT CAG TCC CTG GAG TGT CCC TGA GGAAGGCCCT TAATACCTCC 200
62 Arg Gly Asn Leu Gln Ser Leu Glu Cys Pro *
63 45 50
64
65 TTCTTAATAC CATGCTGCAG AGCAGGGGCAC ATCCTAGCCC AGGAGAAGTG GCCAGCACAA 260
66 TCCAATCAAA TCGTTGCAAA TCAGATTACA CTGTGCATGT CCTAGGAAAG GGAATCTTTA 320
67 CAAAATAAAC AGTGTGGACC CCTCAAAAAA AAAAAAAGC CGAATTC 367
68
69 (2) INFORMATION FOR SEQ ID NO:2:
70 (i) SEQUENCE CHARACTERISTICS:
71 (A) LENGTH: 52 amino acids
72 (B) TYPE: amino acid
73 (D) TOPOLOGY: linear
74 (ii) MOLECULE TYPE: protein
75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
76 Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn Ser
77 1 5 10 15
78 Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg Asn Ser Lys Met
79 20 25 30
80 Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe Arg Gly Asn Leu Gln Ser
81 35 40 45
82 Leu Glu Cys Pro
83 50
84
85 (2) INFORMATION FOR SEQ ID NO:3:
86 (i) SEQUENCE CHARACTERISTICS:
87 (A) LENGTH: 1382 base pairs
88 (B) TYPE: nucleic acid
89 (C) STRANDEDNESS: double
90 (D) TOPOLOGY: linear
91 (ii) MOLECULE TYPE: cDNA
92 (ix) FEATURE:
93 (A) NAME/KEY: CDS
94 (B) LOCATION: 312..1370
95 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
96 GAATTCGGCT TCTACTACTA CTAGGCCACG CGTCGCCTAG TACGGGGGGG GGGGGGGGGG 60
97 TCAGCGAGTC CTTGCCCTCCC GGCGGCTCAG GACGAGGGCA GATCTCGTTC TGGGGCAAGC 120
98 CGTTGACACT CGTCCCTGTC CACCGCCCGG GCTCCGTGCC GCCAAGTTTT CATTTTCCAC 180
99 CTTCTCTGCC TCCAGTCCCC CAGCCCCTGG CCGAGAGAAG GGTCTTACCG GCCGGGATTG 240

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100	CTGGAAACAC CAAGAGGTGG TTTTGTGTTT TTAAAACTTC TGTTTCTTGG GAGGGGGTGT	300
101	GGCGGGGCAG G ATG AGC AAC TCC GTT CCT CTG CTC TGT TTC TGG AGC CTC	350
102	Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu	
103	55 60 65	
104	TGC TAT TGC TTT GCT GCG GGG AGC CCC GTA CCT TTT GGT CCA GAG GGA	398
105	Cys Tyr Cys Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly	
106	70 75 80	
107	CGG CTG GAA GAT AAG CTC CAC AAA CCC AAA GCT ACA CAG ACT GAG GTC	446
108	Arg Leu Glu Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val	
109	85 90 95	
110	AAA CCA TCT GTG AGG TTT AAC CTC CGC ACC TCC AAG GAC CCA GAG CAT	494
111	Lys Pro Ser Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu His	
112	100 105 110	
113	GAA GGA TGC TAC CTC TCC GTC GGC CAC AGC CAG CCC TTA GAA GAC TGC	542
114	Glu Gly Cys Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu Asp Cys	
115	115 120 125 130	
116	AGT TTC AAC ATG ACA GCT AAA ACC TTT TTC ATC ATT CAC GGA TGG ACG	590
117	Ser Phe Asn Met Thr Ala Lys Thr Phe Phe Ile Ile His Gly Trp Thr	
118	135 140 145	
119	ATG AGC GGT ATC TTT GAA AAC TGG CTG CAC AAA CTC GTG TCA GCC CTG	638
120	Met Ser Gly Ile Phe Glu Asn Trp Leu His Lys Leu Val Ser Ala Leu	
121	150 155 160	
122	CAC ACA AGA GAG AAA GAC GCC AAT GTA GTT GTG GTT GAC TGG CTC CCC	686
123	His Thr Arg Glu Lys Asp Ala Asn Val Val Val Val Asp Trp Leu Pro	
124	165 170 175	
125	CTG GCC CAC CAG CTT TAC ACG GAT GCG GTC AAT AAT ACC AGG GTG GTG	734
126	Leu Ala His Gln Leu Tyr Thr Asp Ala Val Asn Asn Thr Arg Val Val	
127	180 185 190	
128	GGA CAC AGC ATT GCC AGG ATG CTC GAC TGG CTG CAG GAG AAG GAC GAT	782
129	Gly His Ser Ile Ala Arg Met Leu Asp Trp Leu Gln Glu Lys Asp Asp	
130	195 200 205 210	
131	TTT TCT CTC GGG AAT GTC CAC TTG ATC GGC TAC AGC CTC GGA GCG CAC	830
132	Phe Ser Leu Gly Asn Val His Leu Ile Gly Tyr Ser Leu Gly Ala His	
133	215 220 225	
134	GTG GCC GGG TAT GCA GGC AAC TTC GTG AAA GGA ACG GTG GGC CGA ATC	878
135	Val Ala Gly Tyr Ala Gly Asn Phe Val Lys Gly Thr Val Gly Arg Ile	
136	230 235 240	
137	ACA GGT TTG GAT CCT GCC GGG CCC ATG TTT GAA GGG GCC GAC ATC CAC	926
138	Thr Gly Leu Asp Pro Ala Gly Pro Met Phe Glu Gly Ala Asp Ile His	
139	245 250 255	
140	AAG AGG CTC TCT CCG GAC GAT GCA GAT TTT GTG GAT GTC CTC CAC ACC	974
141	Lys Arg Leu Ser Pro Asp Asp Ala Asp Phe Val Asp Val Leu His Thr	
142	260 265 270	
143	TAC ACG CGT TCC TTC GGC TTG AGC ATT GGT ATT CAG ATG CCT GTG GGC	1022
144	Tyr Thr Arg Ser Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly	
145	275 280 285 290	
146	CAC ATT GAC ATC TAC CCC AAT GGG GGT GAC TTC CAG CCA GGC TGT GGA	1070
147	His Ile Asp Ile Tyr Pro Asn Gly Gly Asp Phe Gln Pro Gly Cys Gly	
148	295 300 305	
149	CTC AAC GAT GTC TTG GGA TCA ATT GCA TAT GGA ACA ATC ACA GAG GTG	1118
150	Leu Asn Asp Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val	
151	310 315 320	
152	GTA AAA TGT GAG CAT GAG CGA GCC GTC CAC CTC TTT GTT GAC TCT CTG	1166

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153 Val Lys Cys Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu
154      325      330      335
155 GTG AAT CAG GAC AAG CCG AGT TTT GCC TTC CAG TGC ACT GAC TCC AAT      1214
156 Val Asn Gln Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser Asn
157      340      345      350
158 CGC TTC AAA AAG GGG ATC TGT CTG AGC TGC CGC AAG AAC CGT TGT AAT      1262
159 Arg Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn
160      355      360      365      370
161 AGC ATT GGC TAC AAT GCC AAG AAA ATG AGG AAC AAG AGG AAC AGC AAA      1310
162 Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg Asn Ser Lys
163      375      380      385
164 ATG TAC CTA AAA ACC CGG GCA GGC ATG CCT TTC AGA GGT AAC CTT CAG      1358
165 Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe Arg Gly Asn Leu Gln
166      390      395      400
167 TCC CTG GAG TGT CAAGCCGAAT TC      1382
168 Ser Leu Glu Cys
169      405
170

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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178 Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys Tyr Cys
179   1      5      10      15
180 Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg Leu Glu
181      20      25      30
182 Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val Lys Pro Ser
183      35      40      45
184 Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu His Glu Gly Cys
185      50      55      60
186 Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu Asp Cys Ser Phe Asn
187      65      70      75      80
188 Met Thr Ala Lys Thr Phe Phe Ile Ile His Gly Trp Thr Met Ser Gly
189      85      90      95
190 Ile Phe Glu Asn Trp Leu His Lys Leu Val Ser Ala Leu His Thr Arg
191      100      105      110
192 Glu Lys Asp Ala Asn Val Val Val Val Asp Trp Leu Pro Leu Ala His
193      115      120      125
194 Gln Leu Tyr Thr Asp Ala Val Asn Asn Thr Arg Val Val Gly His Ser
195      130      135      140
196 Ile Ala Arg Met Leu Asp Trp Leu Gln Glu Lys Asp Asp Phe Ser Leu
197      145      150      155      160
198 Gly Asn Val His Leu Ile Gly Tyr Ser Leu Gly Ala His Val Ala Gly
199      165      170      175
200 Tyr Ala Gly Asn Phe Val Lys Gly Thr Val Gly Arg Ile Thr Gly Leu
201      180      185      190
202 Asp Pro Ala Gly Pro Met Phe Glu Gly Ala Asp Ile His Lys Arg Leu
203      195      200      205
204 Ser Pro Asp Asp Ala Asp Phe Val Asp Val Leu His Thr Tyr Thr Arg
205      210      215      220

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206 Ser Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly His Ile Asp
207 225 230 235 240
208 Ile Tyr Pro Asn Gly Gly Asp Phe Gln Pro Gly Cys Gly Leu Asn Asp
209 245 250 255
210 Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val Val Lys Cys
211 260 265 270
212 Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu Val Asn Gln
213 275 280 285
214 Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser Asn Arg Phe Lys
215 290 295 300
216 Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn Ser Ile Gly
217 305 310 315 320
218 Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg Asn Ser Lys Met Tyr Leu
219 325 330 335
220 Lys Thr Arg Ala Gly Met Pro Phe Arg Gly Asn Leu Gln Ser Leu Glu
221 340 345 350
222 Cys
223

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
226 (A) LENGTH: 1065 base pairs
227 (B) TYPE: nucleic acid
228 (C) STRANDEDNESS: double
229 (D) TOPOLOGY: linear
230 (ii) MOLECULE TYPE: cDNA
231 (ix) FEATURE:
232 (A) NAME/KEY: CDS
233 (B) LOCATION: 1..1065
234 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

235	ATG AGC AAC TCC GTT CCT CTG CTC TGT TTC TGG AGC CTC TGC TAT TGC	48
236	Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys Tyr Cys	
237	355 360 365	
238	TTT GCT GCG GGG AGC CCC GTA CCT TTT GGT CCA GAG GGA CGG CTG GAA	96
239	Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg Leu Glu	
240	370 375 380 385	
241	GAT AAG CTC CAC AAA CCC AAA GCT ACA CAG ACT GAG GTC AAA CCA TCT	144
242	Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val Lys Pro Ser	
243	390 395 400	
244	GTG AGG TTT AAC CTC CGC ACC TCC AAG GAC CCA GAG CAT GAA GGA TGC	192
245	Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu His Glu Gly Cys	
246	405 410 415	
247	TAC CTC TCC GTC GGC CAC AGC CAG CCC TTA GAA GAC TGC AGT TTC AAC	240
248	Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu Asp Cys Ser Phe Asn	
249	420 425 430	
250	ATG ACA GCT AAA ACC TTT TTC ATC ATT CAC GGA TGG ACG ATG AGC GGT	288

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SEQUENCE VERIFICATION REPORT
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Line

Error

Original Text